

=====

Sequence Listing was accepted with existing errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Thu Jul 26 15:13:52 EDT 2007

=====

=====

Sequence Listing was accepted with existing errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: markspencer

Timestamp: Fri Jul 13 08:23:43 EDT 2007

=====

Application No: 10576281 Version No: 2.1

Input Set:

Output Set:

Started: 2007-07-13 08:23:22.883
Finished: 2007-07-13 08:23:23.171
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 288 ms
Total Warnings: 1
Total Errors: 0
No. of SeqIDs Defined: 21
Actual SeqID Count: 21

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (21)

SEQUENCE LISTING

<110> Toshihiro NAKAJIMA
Tetsuya AMANO
Lei ZHANG
Rie IKEDA
Satoshi YAMASAKI
Naoko YAGISHITA

<120> Method of inhibiting secretase activity

<130> L7350.0007

<140> 10576281

<141> 2007-07-06

<150> PCT/JP2004/015950

<151> 2004-10-20

<150> JP2003-359704

<151> 2003-10-20

<160> 21

<170> PatentIn version 3.4

<210> 1

<211> 3374

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (403)..(2256)

<400> 1

gccctttctt atgagcatgc ctgtgttggg ttgacagtga gggtaataat gacttgttgg 60

ttgattttagt atatagggct ctcccttgca aggttaattag gtccttaaa ttacctgtaa 120

gattttcttg ccacagcatc cattctggtt aggctggtga tcttctgagt agtgatagat 180

tggttggtgg tgaggtttac aggtgttccc ttctcttact cctgggttgg gctacaatca 240

ggtggcgtct agagcagcat gggacaggtg ggttaaggggca gtcttctcat tatgcagaag 300

tgtatcaactt aaatctctgt cagatctacc tttatgttagc ccggcagtcg cgcggattga 360

gcggggctcgc ggcgctgggt tcctggtctc cggggccaggg ca atg ttc cgc acg 414

Met Phe Arg Thr

1

gca gtg atg atg gcg gcc agc ctg gcg ctg acc ggg gct gtg gtg gct 462

Ala Val Met Met Ala Ala Ser Leu Ala Leu Thr Gly Ala Val Val Ala

cac gcc tac tac ctc aaa cac cag ttc tac ccc act gtg gtg tac ctg		510	
His Ala Tyr Tyr Leu Lys His Gln Phe Tyr Pro Thr Val Val Tyr Leu			
25	30	35	
acc aag tcc agc ccc agc atg gca gtc ctg tac atc cag gcc ttt gtc		558	
Thr Lys Ser Ser Pro Ser Met Ala Val Leu Tyr Ile Gln Ala Phe Val			
40	45	50	
ctt gtc ttc ctt ctg ggc aag gtg atg ggc aag gtg ttc ttt ggg caa		606	
Leu Val Phe Leu Leu Gly Lys Val Met Gly Lys Val Phe Phe Gly Gln			
55	60	65	
ctg agg gca gca gag atg gag cac ctt ctg gaa cgt tcc tgg tac gcc		654	
Leu Arg Ala Ala Glu Met Glu His Leu Leu Glu Arg Ser Trp Tyr Ala			
70	75	80	
gtc aca gag act tgt ctg gcc ttc acc gtt ttt cgg gat gac ttc agc		702	
Val Thr Glu Thr Cys Leu Ala Phe Thr Val Phe Arg Asp Asp Phe Ser			
85	90	95	100
ccc cgc ttt gtt gca ctc ttc act ctt ctt ctc ttc ctc aaa tgt ttc		750	
Pro Arg Phe Val Ala Leu Phe Thr Leu Leu Leu Phe Leu Lys Cys Phe			
105	110	115	
cac tgg ctg gct gag gac cgt gtg gac ttt atg gaa cgc agc ccc aac		798	
His Trp Leu Ala Glu Asp Arg Val Asp Phe Met Glu Arg Ser Pro Asn			
120	125	130	
atc tcc tgg ctc ttt cac tgc cgc att gtc tct ctt atg ttc ctc ctg		846	
Ile Ser Trp Leu Phe His Cys Arg Ile Val Ser Leu Met Phe Leu Leu			
135	140	145	
ggc atc ctg gac ttc ctc ttc gtc agc cac gcc tat cac agc atc ctg		894	
Gly Ile Leu Asp Phe Leu Phe Val Ser His Ala Tyr His Ser Ile Leu			
150	155	160	
acc cgt ggg gcc tct gtg cag ctg gtg ttt ggc ttt gag tat gcc atc		942	
Thr Arg Gly Ala Ser Val Gln Leu Val Phe Gly Phe Glu Tyr Ala Ile			
165	170	175	180
ctg atg acg atg gtg ctc acc atc ttc atc aag tat gtg ctg cac tcc		990	
Leu Met Thr Met Val Leu Thr Ile Phe Ile Lys Tyr Val Leu His Ser			
185	190	195	
gtg gac ctc cag agt gag aac ccc tgg gac aac aag gct gtg tac atg		1038	
Val Asp Leu Gln Ser Glu Asn Pro Trp Asp Asn Lys Ala Val Tyr Met			
200	205	210	
ctc tac aca gag ctg ttt aca ggc ttc atc aag gtt ctg ctg tac atg		1086	
Leu Tyr Thr Glu Leu Phe Thr Gly Phe Ile Lys Val Leu Leu Tyr Met			
215	220	225	
gcc ttc atg acc atc atg atc aag gtg cac acc ttc cca ctc ttt gcc		1134	
Ala Phe Met Thr Ile Met Ile Lys Val His Thr Phe Pro Leu Phe Ala			
230	235	240	
atc cgg ccc atg tac ctg gcc atg aga cag ttc aag aaa gct gtg aca		1182	

Ile Arg Pro Met Tyr Leu Ala Met Arg Gln Phe Lys Lys Ala Val Thr			
245	250	255	260
gat gcc atc atg tct cgc cga gcc atc cgc aac atg aac acc acc ctg tat			1230
Asp Ala Ile Met Ser Arg Arg Ala Ile Arg Asn Met Asn Thr Leu Tyr			
265	270	275	
cca gat gcc acc cca gag gag ctc cag gca atg gac aat gtc tgc atc			1278
Pro Asp Ala Thr Pro Glu Glu Leu Gln Ala Met Asp Asn Val Cys Ile			
280	285	290	
atc tgc cga gaa gag atg gtg act ggt gcc aag aga ctg ccc tgc aac			1326
Ile Cys Arg Glu Glu Met Val Thr Gly Ala Lys Arg Leu Pro Cys Asn			
295	300	305	
cac att ttc cat acc agc tgc ctg cgc tcc tgg ttc cag cgg cag cag			1374
His Ile Phe His Thr Ser Cys Leu Arg Ser Trp Phe Gln Arg Gln Gln			
310	315	320	
acc tgc ccc acc tgc cgt atg gat gtc ctt cgt gca tcg ctg cca gcc			1422
Thr Cys Pro Thr Cys Arg Met Asp Val Leu Arg Ala Ser Leu Pro Ala			
325	330	335	340
cag tca cca cca ccc ccg gag cct gcg gat cag ggg cca ccc cct gcc			1470
Gln Ser Pro Pro Pro Pro Glu Pro Ala Asp Gln Gly Pro Pro Pro Ala			
345	350	355	
ccc cac ccc cca cca ctc ttg cct cag ccc ccc aac ttc ccc cag ggc			1518
Pro His Pro Pro Leu Leu Pro Gln Pro Pro Asn Phe Pro Gln Gly			
360	365	370	
ctc ctg cct ttt cct cca ggc atg ttc cca ctg tgg ccc ccc atg			1566
Leu Leu Pro Pro Phe Pro Pro Gly Met Phe Pro Leu Trp Pro Pro Met			
375	380	385	
ggc ccc ttt cca cct gtc ccg cct ccc ccc agc tca gga gag gct gtg			1614
Gly Pro Phe Pro Pro Val Pro Pro Pro Ser Ser Gly Glu Ala Val			
390	395	400	
gct cct cca tcc acc agt gca gca gcc ctt tct cgg ccc agt gga gca			1662
Ala Pro Pro Ser Thr Ser Ala Ala Leu Ser Arg Pro Ser Gly Ala			
405	410	415	420
gct aca acc aca gct gct ggc acc agt gct act gct gct tct gcc aca			1710
Ala Thr Thr Thr Ala Ala Gly Thr Ser Ala Thr Ala Ala Ser Ala Thr			
425	430	435	
gca tct ggc cca ggc tct ggc tct gcc cca gag gct ggc cct gcc cct			1758
Ala Ser Gly Pro Gly Ser Gly Ser Ala Pro Glu Ala Gly Pro Ala Pro			
440	445	450	
ggt ttc ccc ttc cct ccc tgg atg ggt atg ccc ctg cct cca ccc			1806
Gly Phe Pro Phe Pro Pro Trp Met Gly Met Pro Leu Pro Pro Pro			
455	460	465	
ttt gcc ttc ccc cca atg cct gtg ccc cct gcg ggc ttt gct ggg ctg			1854
Phe Ala Phe Pro Pro Met Pro Val Pro Pro Ala Gly Phe Ala Gly Leu			

470	475	480	
acc cca gag gag cta cga gct ctg gag ggc cat gag cgg cag cac ctg			1902
Thr Pro Glu Glu Leu Arg Ala Leu Glu Gly His Glu Arg Gln His Leu			
485	490	495	500
gag gcc cgg ctg cag agc ctg cgt aac atc cac aca ctg ctg gac gcc			1950
Glu Ala Arg Leu Gln Ser Leu Arg Asn Ile His Thr Leu Leu Asp Ala			
505	510	515	
gcc atg ctg cag atc aac cag tac ctc acc gtg ctg gcc tcc ttg ggg			1998
Ala Met Leu Gln Ile Asn Gln Tyr Leu Thr Val Leu Ala Ser Leu Gly			
520	525	530	
ccc ccc cgg cct gcc act tca gtc aac tcc act gag ggg act gcc act			2046
Pro Pro Arg Pro Ala Thr Ser Val Asn Ser Thr Glu Gly Thr Ala Thr			
535	540	545	
aca gtt gtt gct gct gcc tcc tcc acc agc atc cct agc tca gag gcc			2094
Thr Val Val Ala Ala Ala Ser Ser Thr Ser Ile Pro Ser Ser Glu Ala			
550	555	560	
acg acc cca acc cca gga gcc tcc cca cca gcc cct gaa atg gaa agg			2142
Thr Thr Pro Thr Pro Gly Ala Ser Pro Pro Ala Pro Glu Met Glu Arg			
565	570	575	580
cct cca gct cct gag tca gtg ggc aca gag gag atg cct gag gat gga			2190
Pro Pro Ala Pro Glu Ser Val Gly Thr Glu Glu Met Pro Glu Asp Gly			
585	590	595	
gag ccc gat gca gca gag ctc cgc cgg cgc ctg cag aag ctg gag			2238
Glu Pro Asp Ala Ala Glu Leu Arg Arg Arg Arg Leu Gln Lys Leu Glu			
600	605	610	
tct cct gtt gcc cac tga cactgccccca gcccagcccc agcctctgct			2286
Ser Pro Val Ala His			
615			
ctttttagca gccctcgctg gaacatgtcc tgccaccaag tgccagctcc ctctctgtct			2346
gcaccaggaa gtagtacccc cagctctgag aaagaggcgg catcccctag gccaagtggaa			2406
aagaggctgg ggttccatt tgactccagt cccaggcagc catggggatc tcgggtcagt			2466
tccagccttc ctctccaact cttcagccct gtgttctgct gggccatga aggcagaagg			2526
ttagcctct gagaagccct cttttcccc caccccttcc caggagaagg ggctgcccct			2586
ccaagcccta cttgtatgtc cggagtaca ctgcagtgcc gaacagtatt agctccgtt			2646
cccaagtgtg gactccagag gggctggagg caagctatga acttgctcgc tggccacccc			2706
ctaagactgg taccatttc ctttttttac cctgatctcc ccagaaggct cttgtggtg			2766
tggctgtgcc ccctatgccc tgtggcattt ctgcgtctta ctggcaacca cacaactcag			2826
ggaaaggaat gcctggagt gggggtgcaag gcggggcagca ctgagggacc ctgccccgcc			2886

cctcccccca ggccccttc ccctgcagct tctcaagtga gactgacctg tctcacccag	2946
cagccactgc ccagccgcac tccaggcaag ggccagtgcg cctgctcctg accactgcaa	3006
tcccagcgcc caaggaaggc cacttctcaa ctggcagaac ttctgaagtt tagaattgga	3066
attacttcct tactagtgtc ttttggctta aattttgtct tttgaagttg aatgcttaat	3126
cccgaaaag aggaacagga gtgccagact cctggcttt ccagttaga aaaggctcg	3186
tgcctaggag ggaccacagg agctgggacc tgcctgcccc tgcctttcc cttgggttt	3246
gtgttacaag agtttttggaa gacagttca gatgattatt taattttaaa atattgtaca	3306
aattttataa gcttaaatttggatatacagc caaataaaaaa cttgcattaa caaaaaaaaaa	3366
aaaaaaaaa	3374

<210> 2
<211> 617
<212> PRT
<213> Homo sapiens

<400> 2

Met Phe Arg Thr Ala Val Met Met Ala Ala Ser Leu Ala Leu Thr Gly			
1	5	10	15

Ala Val Val Ala His Ala Tyr Tyr Leu Lys His Gln Phe Tyr Pro Thr		
20	25	30

Val Val Tyr Leu Thr Lys Ser Ser Pro Ser Met Ala Val Leu Tyr Ile		
35	40	45

Gln Ala Phe Val Leu Val Phe Leu Leu Gly Lys Val Met Gly Lys Val		
50	55	60

Phe Phe Gly Gln Leu Arg Ala Ala Glu Met Glu His Leu Leu Glu Arg			
65	70	75	80

Ser Trp Tyr Ala Val Thr Glu Thr Cys Leu Ala Phe Thr Val Phe Arg		
85	90	95

Asp Asp Phe Ser Pro Arg Phe Val Ala Leu Phe Thr Leu Leu Phe		
100	105	110

Leu Lys Cys Phe His Trp Leu Ala Glu Asp Arg Val Asp Phe Met Glu		
115	120	125

Arg Ser Pro Asn Ile Ser Trp Leu Phe His Cys Arg Ile Val Ser Leu
130 135 140

Met Phe Leu Leu Gly Ile Leu Asp Phe Leu Phe Val Ser His Ala Tyr
145 150 155 160

His Ser Ile Leu Thr Arg Gly Ala Ser Val Gln Leu Val Phe Gly Phe
165 170 175

Glu Tyr Ala Ile Leu Met Thr Met Val Leu Thr Ile Phe Ile Lys Tyr
180 185 190

Val Leu His Ser Val Asp Leu Gln Ser Glu Asn Pro Trp Asp Asn Lys
195 200 205

Ala Val Tyr Met Leu Tyr Thr Glu Leu Phe Thr Gly Phe Ile Lys Val
210 215 220

Leu Leu Tyr Met Ala Phe Met Thr Ile Met Ile Lys Val His Thr Phe
225 230 235 240

Pro Leu Phe Ala Ile Arg Pro Met Tyr Leu Ala Met Arg Gln Phe Lys
245 250 255

Lys Ala Val Thr Asp Ala Ile Met Ser Arg Arg Ala Ile Arg Asn Met
260 265 270

Asn Thr Leu Tyr Pro Asp Ala Thr Pro Glu Glu Leu Gln Ala Met Asp
275 280 285

Asn Val Cys Ile Ile Cys Arg Glu Glu Met Val Thr Gly Ala Lys Arg
290 295 300

Leu Pro Cys Asn His Ile Phe His Thr Ser Cys Leu Arg Ser Trp Phe
305 310 315 320

Gln Arg Gln Gln Thr Cys Pro Thr Cys Arg Met Asp Val Leu Arg Ala
325 330 335

Ser Leu Pro Ala Gln Ser Pro Pro Pro Pro Glu Pro Ala Asp Gln Gly
340 345 350

Pro Pro Pro Ala Pro His Pro Pro Pro Leu Leu Pro Gln Pro Pro Asn
355 360 365

Phe Pro Gln Gly Leu Leu Pro Pro Phe Pro Pro Gly Met Phe Pro Leu
370 375 380

Trp Pro Pro Met Gly Pro Phe Pro Pro Val Pro Pro Pro Pro Ser Ser
385 390 395 400

Gly Glu Ala Val Ala Pro Pro Ser Thr Ser Ala Ala Ala Leu Ser Arg
405 410 415

Pro Ser Gly Ala Ala Thr Thr Ala Ala Gly Thr Ser Ala Thr Ala
420 425 430

Ala Ser Ala Thr Ala Ser Gly Pro Gly Ser Gly Ser Ala Pro Glu Ala
435 440 445

Gly Pro Ala Pro Gly Phe Pro Phe Pro Pro Pro Trp Met Gly Met Pro
450 455 460

Leu Pro Pro Pro Phe Ala Phe Pro Pro Met Pro Val Pro Pro Ala Gly
465 470 475 480

Phe Ala Gly Leu Thr Pro Glu Glu Leu Arg Ala Leu Glu Gly His Glu
485 490 495

Arg Gln His Leu Glu Ala Arg Leu Gln Ser Leu Arg Asn Ile His Thr
500 505 510

Leu Leu Asp Ala Ala Met Leu Gln Ile Asn Gln Tyr Leu Thr Val Leu
515 520 525

Ala Ser Leu Gly Pro Pro Arg Pro Ala Thr Ser Val Asn Ser Thr Glu
530 535 540

Gly Thr Ala Thr Thr Val Val Ala Ala Ser Ser Thr Ser Ile Pro
545 550 555 560

Ser Ser Glu Ala Thr Thr Pro Thr Pro Gly Ala Ser Pro Pro Ala Pro
565 570 575

Glu Met Glu Arg Pro Pro Ala Pro Glu Ser Val Gly Thr Glu Glu Met
580 585 590

Pro Glu Asp Gly Glu Pro Asp Ala Ala Glu Leu Arg Arg Arg Arg Leu
595 600 605

Gln Lys Leu Glu Ser Pro Val Ala His
610 615

<210> 3
<211> 23
<212> DNA
<213> Homo sapiens

<400> 3
aatgtctgca tcatctgccg aga 23

<210> 4
<211> 23
<212> DNA
<213> Homo sapiens

<400> 4
aagctgtgac agatgccatc atg 23

<210> 5
<211> 23
<212> DNA
<213> Homo sapiens

<400> 5
aaagctgtga cagatccat cat 23

<210> 6
<211> 23
<212> DNA
<213> Homo sapiens

<400> 6
aagaaagctg tgacagatgc cat 23

<210> 7
<211> 23
<212> DNA
<213> Homo sapiens

<400> 7
aaggttctgc tgtacatggc ctt 23

<210> 8
<211> 23
<212> DNA
<213> Homo sapiens

<400> 8
aacaaggctg tgtacatgct cta

23

<210> 9
<211> 23
<212> DNA
<213> Homo sapiens

<400> 9
aaatgtttcc actggctggc tga

23

<210> 10
<211> 23
<212> DNA
<213> Homo sapiens

<400> 10
aagggtgttct ttgggcaact gag

SEQUENCE LISTING

<110> Toshihiro NAKAJIMA
Tetsuya AMANO
Lei ZHANG
Rie IKEDA
Satoshi YAMASAKI
Naoko YAGISHITA

<120> Method of inhibiting secretase activity

<130> L7350.0007

<140> 10576281

<141> 2007-07-06

<150> PCT/JP2004/015950

<151> 2004-10-20

<150> JP2003-359704

<151> 2003-10-20

<160> 21

<170> PatentIn version 3.4

<210> 1

<211> 3374

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (403)..(2256)

<400> 1

gccctttctt atgagcatgc ctgtgttggg ttgacagtga gggtaataat gacttgttgg 60

ttgattttagt atatagggct ctcccttgca aggttaattag gtccttaaa ttacctgtaa 120

gattttcttg ccacagcatc cattctggtt aggctggtga tcttctgagt agtgatagat 180

tggttggtgg tgaggtttac aggtgttccc ttctcttact cctgggttgg gctacaatca 240

ggtggcgtct agagcagcat gggacaggtg ggttaaggggca gtcttctcat tatgcagaag 300

tgtatcaactt aaatctctgt cagatctacc tttatgttagc ccggcagtcg cgcggattga 360

gcggggctcgc ggcgctgggt tcctggtctc cggggccaggg ca atg ttc cgc acg 414

Met Phe Arg Thr

1

gca gtg atg atg gcg gcc agc ctg gcg ctg acc ggg gct gtg gtg gct 462

Ala Val Met Met Ala Ala Ser Leu Ala Leu Thr Gly Ala Val Val Ala

5 10 15 20

cac gcc tac tac ctc aaa cac cag ttc tac ccc act gtg gtg tac ctg		510	
His Ala Tyr Tyr Leu Lys His Gln Phe Tyr Pro Thr Val Val Tyr Leu			
25	30	35	
acc aag tcc agc ccc agc atg gca gtc ctg tac atc cag gcc ttt gtc		558	
Thr Lys Ser Ser Pro Ser Met Ala Val Leu Tyr Ile Gln Ala Phe Val			
40	45	50	
ctt gtc ttc ctt ctg ggc aag gtg atg ggc aag gtg ttc ttt ggg caa		606	
Leu Val Phe Leu Leu Gly Lys Val Met Gly Lys Val Phe Phe Gly Gln			
55	60	65	
ctg agg gca gca gag atg gag cac ctt ctg gaa cgt tcc tgg tac gcc		654	
Leu Arg Ala Ala Glu Met Glu His Leu Leu Glu Arg Ser Trp Tyr Ala			
70	75	80	
gtc aca gag act tgt ctg gcc ttc acc gtt ttt cgg gat gac ttc agc		702	
Val Thr Glu Thr Cys Leu Ala Phe Thr Val Phe Arg Asp Asp Phe Ser			
85	90	95	100
ccc cgc ttt gtt gca ctc ttc act ctt ctt ctc ttc ctc aaa tgt ttc		750	
Pro Arg Phe Val Ala Leu Phe Thr Leu Leu Leu Phe Leu Lys Cys Phe			
105	110	115	
cac tgg ctg gct gag gac cgt gtg gac ttt atg gaa cgc agc ccc aac		798	
His Trp Leu Ala Glu Asp Arg Val Asp Phe Met Glu Arg Ser Pro Asn			
120	125	130	
atc tcc tgg ctc ttt cac tgc cgc att gtc tct ctt atg ttc ctc ctg		846	
Ile Ser Trp Leu Phe His Cys Arg Ile Val Ser Leu Met Phe Leu Leu			
135	140	145	
ggc atc ctg gac ttc ctc ttc gtc agc cac gcc tat cac agc atc ctg		894	
Gly Ile Leu Asp Phe Leu Phe Val Ser His Ala Tyr His Ser Ile Leu			
150	155	160	
acc cgt ggg gcc tct gtg cag ctg gtg ttt ggc ttt gag tat gcc atc		942	
Thr Arg Gly Ala Ser Val Gln Leu Val Phe Gly Phe Glu Tyr Ala Ile			
165	170	175	180
ctg atg acg atg gtg ctc acc atc ttc atc aag tat gtg ctg cac tcc		990	
Leu Met Thr Met Val Leu Thr Ile Phe Ile Lys Tyr Val Leu His Ser			
185	190	195	
gtg gac ctc cag agt gag aac ccc tgg gac aac aag gct gtg tac atg		1038	
Val Asp Leu Gln Ser Glu Asn Pro Trp Asp Asn Lys Ala Val Tyr Met			
200	205	210	
ctc tac aca gag ctg ttt aca ggc ttc atc aag gtt ctg ctg tac atg		1086	
Leu Tyr Thr Glu Leu Phe Thr Gly Phe Ile Lys Val Leu Leu Tyr Met			
215	220	225	
gcc ttc atg acc atc atg atc aag gtg cac acc ttc cca ctc ttt gcc		1134	
Ala Phe Met Thr Ile Met Ile Lys Val His Thr Phe Pro Leu Phe Ala			
230	235	240	
atc cgg ccc atg tac ctg gcc atg aga cag ttc aag aaa gct gtg aca		1182	

Ile Arg Pro Met Tyr Leu Ala Met Arg Gln Phe Lys Lys Ala Val Thr			
245	250	255	260
gat gcc atc atg tct cgc cga gcc atc cgc aac atg aac acc acc ctg tat			1230
Asp Ala Ile Met Ser Arg Arg Ala Ile Arg Asn Met Asn Thr Leu Tyr			
265	270	275	
cca gat gcc acc cca gag gag ctc cag gca atg gac aat gtc tgc atc			1278
Pro Asp Ala Thr Pro Glu Glu Leu Gln Ala Met Asp Asn Val Cys Ile			
280	285	290	
atc tgc cga gaa gag atg gtg act ggt gcc aag aga ctg ccc tgc aac			1326
Ile Cys Arg Glu Glu Met Val Thr Gly Ala Lys Arg Leu Pro Cys Asn			
295	300	305	
cac att ttc cat acc agc tgc ctg cgc tcc tgg ttc cag cgg cag cag			1374
His Ile Phe His Thr Ser Cys Leu Arg Ser Trp Phe Gln Arg Gln Gln			
310	315	320	
acc tgc ccc acc tgc cgt atg gat gtc ctt cgt gca tcg ctg cca gcc			1422
Thr Cys Pro Thr Cys Arg Met Asp Val Leu Arg Ala Ser Leu Pro Ala			
325	330	335	340
cag tca cca cca ccc ccg gag cct gcg gat cag ggg cca ccc cct gcc			1470
Gln Ser Pro Pro Pro Pro Glu Pro Ala Asp Gln Gly Pro Pro Pro Ala			
345	350	355	
ccc cac ccc cca cca ctc ttg cct cag ccc ccc aac ttc ccc cag ggc			1518
Pro His Pro Pro Leu Leu Pro Gln Pro Pro Asn Phe Pro Gln Gly			
360	365	370	
ctc ctg cct ttt cct cca ggc atg ttc cca ctg tgg ccc ccc atg			1566
Leu Leu Pro Pro Phe Pro Pro Gly Met Phe Pro Leu Trp Pro Pro Met			
375	380	385	
ggc ccc ttt cca cct gtc ccg cct ccc ccc agc tca gga gag gct gtg			1614
Gly Pro Phe Pro Pro Val Pro Pro Pro Ser Ser Gly Glu Ala Val			
390	395	400	
gct cct cca tcc acc agt gca gca gcc ctt tct cgg ccc agt gga gca			1662
Ala Pro Pro Ser Thr Ser Ala Ala Leu Ser Arg Pro Ser Gly Ala			
405	410	415	420
gct aca acc aca gct gct ggc acc agt gct act gct gct tct gcc aca			1710
Ala Thr Thr Thr Ala Ala Gly Thr Ser Ala Thr Ala Ala Ser Ala Thr			
425	430	435	
gca tct ggc cca ggc tct ggc tct gcc cca gag gct ggc cct gcc cct			1758
Ala Ser Gly Pro Gly Ser Gly Ser Ala Pro Glu Ala Gly Pro Ala Pro			
440	445	450	
ggt ttc ccc ttc cct ccc tgg atg ggt atg ccc ctg cct cca ccc			1806
Gly Phe Pro Phe Pro Pro Trp Met Gly Met Pro Leu Pro Pro Pro			
455	460	465	
ttt gcc ttc ccc cca atg cct gtg ccc cct gcg ggc ttt gct ggg ctg			1854
Phe Ala Phe Pro Pro Met Pro Val Pro Pro Ala Gly Phe Ala Gly Leu			

470	475	480	
acc cca gag gag cta cga gct ctg gag ggc cat gag cgg cag cac ctg			1902
Thr Pro Glu Glu Leu Arg Ala Leu Glu Gly His Glu Arg Gln His Leu			
485	490	495	500
gag gcc cgg ctg cag agc ctg cgt aac atc cac aca ctg ctg gac gcc			1950
Glu Ala Arg Leu Gln Ser Leu Arg Asn Ile His Thr Leu Leu Asp Ala			
505	510	515	
gcc atg ctg cag atc aac cag tac ctc acc gtg ctg gcc tcc ttg ggg			1998
Ala Met Leu Gln Ile Asn Gln Tyr Leu Thr Val Leu Ala Ser Leu Gly			
520	525	530	
ccc ccc cgg cct gcc act tca gtc aac tcc act gag ggg act gcc act			2046
Pro Pro Arg Pro Ala Thr Ser Val Asn Ser Thr Glu Gly Thr Ala Thr			
535	540	545	
aca gtt gtt gct gct gcc tcc tcc acc agc atc cct agc tca gag gcc			2094
Thr Val Val Ala Ala Ala Ser Ser Thr Ser Ile Pro Ser Ser Glu Ala			
550	555	560	
acg acc cca acc cca gga gcc tcc cca cca gcc cct gaa atg gaa agg			2142
Thr Thr Pro Thr Pro Gly Ala Ser Pro Pro Ala Pro Glu Met Glu Arg			
565	570	575	580
cct cca gct cct gag tca gtg ggc aca gag gag atg cct gag gat gga			2190
Pro Pro Ala Pro Glu Ser Val Gly Thr Glu Glu Met Pro Glu Asp Gly			
585	590	595	
gag ccc gat gca gca gag ctc cgc cgg cgc ctg cag aag ctg gag			2238
Glu Pro Asp Ala Ala Glu Leu Arg Arg Arg Arg Leu Gln Lys Leu Glu			
600	605	610	
tct cct gtt gcc cac tga cactgccccca gcccagcccc agcctctgct			2286
Ser Pro Val Ala His			
615			
ctttttagca gccctcgctg gaacatgtcc tgccaccaag tgccagctcc ctctctgtct			2346
gcaccaggaa gtagtacccc cagctctgag aaagaggcgg catcccctag gccaagtggaa			2406
aagaggctgg ggttccatt tgactccagt cccaggcagc catggggatc tcgggtcagt			2466
tccagccttc ctctccaact cttcagccct gtgttctgct gggccatga aggcagaagg			2526
ttagcctct gagaagccct cttttcccc caccccttcc caggagaagg ggctgcccct			2586
ccaagcccta cttgtatgtc cggagtaca ctgcagtgcc gaacagtatt agctccgtt			2646
cccaagtgtg gactccagag gggctggagg caagctatga acttgctcgc tggccacccc			2706
ctaagactgg taccatttc ctttttttac cctgatctcc ccagaaggct cttgtggtg			2766
tggctgtgcc ccctatgccc tgtggcattt ctgcgtctta ctggcaacca cacaactcag			2826
ggaaaggaat gcctggagt gggggtgcaag gcggggcagca ctgagggacc ctgccccgcc			2886

cctcccccca ggccccttc ccctgcagct tctcaagtga gactgacctg tctcacccag	2946
cagccactgc ccagccgcac tccaggcaag ggccagtgcg cctgctcctg accactgcaa	3006
tcccagcgcc caaggaaggc cacttctcaa ctggcagaac ttctgaagtt tagaattgga	3066
attacttcct tactagtgtc ttttggctta aattttgtct tttgaagttg aatgcttaat	3126
cccgaaaag aggaacagga gtgccagact cctggcttt ccagttaga aaaggctcg	3186
tgcctaggag ggaccacagg agctgggacc tgcctgcccc tgcctttcc cttgggttt	3246
gtgttacaag agtttttggaa gacagttca gatgattatt taattttaaa atattgtaca	3306
aattttataa gcttaaatttggatatacagc caaataaaaaa cttgcattaa caaaaaaaaaa	3366
aaaaaaaaa	3374

<210> 2
<211> 617
<212> PRT
<213> Homo sapiens

<400> 2

Met Phe Arg Thr Ala Val Met Met Ala Ala Ser Leu Ala Leu Thr Gly			
1	5	10	15

Ala Val Val Ala His Ala Tyr Tyr Leu Lys His Gln Phe Tyr Pro Thr		
20	25	30

Val Val Tyr Leu Thr Lys Ser Ser Pro Ser Met Ala Val Leu Tyr Ile		
35	40	45

Gln Ala Phe Val Leu Val Phe Leu Leu Gly Lys Val Met Gly Lys Val		
50	55	60

Phe Phe Gly Gln Leu Arg Ala Ala Glu Met Glu His Leu Leu Glu Arg			
65	70	75	80

Ser Trp Tyr Ala Val Thr Glu Thr Cys Leu Ala Phe Thr Val Phe Arg		
85	90	95

Asp Asp Phe Ser Pro Arg Phe Val Ala Leu Phe Thr Leu Leu Phe		
100	105	110

Leu Lys Cys Phe His Trp Leu Ala Glu Asp Arg Val Asp Phe Met Glu		
115	120	125

Arg Ser Pro Asn Ile Ser Trp Leu Phe His Cys Arg Ile Val Ser Leu
130 135 140

Met Phe Leu Leu Gly Ile Leu Asp Phe Leu Phe Val Ser His Ala Tyr
145 150 155 160

His Ser Ile Leu Thr Arg Gly Ala Ser Val Gln Leu Val Phe Gly Phe
165 170 175

Glu Tyr Ala Ile Leu Met Thr Met Val Leu Thr Ile Phe Ile Lys Tyr
180 185 190

Val Leu His Ser Val Asp Leu Gln Ser Glu Asn Pro Trp Asp Asn Lys
195 200 205

Ala Val Tyr Met Leu Tyr Thr Glu Leu Phe Thr Gly Phe Ile Lys Val
210 215 220

Leu Leu Tyr Met Ala Phe Met Thr Ile Met Ile Lys Val His Thr Phe
225 230 235 240

Pro Leu Phe Ala Ile Arg Pro Met Tyr Leu Ala Met Arg Gln Phe Lys
245 250 255

Lys Ala Val Thr Asp Ala Ile Met Ser Arg Arg Ala Ile Arg Asn Met
260 265 270

Asn Thr Leu Tyr Pro Asp Ala Thr Pro Glu Glu Leu Gln Ala Met Asp
275 280 285

Asn Val Cys Ile Ile Cys Arg Glu Glu Met Val Thr Gly Ala Lys Arg
290 295 300

Leu Pro Cys Asn His Ile Phe His Thr Ser Cys Leu Arg Ser Trp Phe
305 310 315 320

Gln Arg Gln Gln Thr Cys Pro Thr Cys Arg Met Asp Val Leu Arg Ala
325 330 335

Ser Leu Pro Ala Gln Ser Pro Pro Pro Pro Glu Pro Ala Asp Gln Gly
340 345 350

Pro Pro Pro Ala Pro His Pro Pro Pro Leu Leu Pro Gln Pro Pro Asn
355 360 365

Phe Pro Gln Gly Leu Leu Pro Pro Phe Pro Pro Gly Met Phe Pro Leu
370 375 380

Trp Pro Pro Met Gly Pro Phe Pro Pro Val Pro Pro Pro Pro Ser Ser
385 390 395 400

Gly Glu Ala Val Ala Pro Pro Ser Thr Ser Ala Ala Ala Leu Ser Arg
405 410 415

Pro Ser Gly Ala Ala Thr Thr Ala Ala Gly Thr Ser Ala Thr Ala
420 425 430

Ala Ser Ala Thr Ala Ser Gly Pro Gly Ser Gly Ser Ala Pro Glu Ala
435 440 445

Gly Pro Ala Pro Gly Phe Pro Phe Pro Pro Pro Trp Met Gly Met Pro
450 455 460

Leu Pro Pro Pro Phe Ala Phe Pro Pro Met Pro Val Pro Pro Ala Gly
465 470 475 480

Phe Ala Gly Leu Thr Pro Glu Glu Leu Arg Ala Leu Glu Gly His Glu
485 490 495

Arg Gln His Leu Glu Ala Arg Leu Gln Ser Leu Arg Asn Ile His Thr
500 505 510

Leu Leu Asp Ala Ala Met Leu Gln Ile Asn Gln Tyr Leu Thr Val Leu
515 520 525

Ala Ser Leu Gly Pro Pro Arg Pro Ala Thr Ser Val Asn Ser Thr Glu
530 535 540

Gly Thr Ala Thr Thr Val Val Ala Ala Ser Ser Thr Ser Ile Pro
545 550 555 560

Ser Ser Glu Ala Thr Thr Pro Thr Pro Gly Ala Ser Pro Pro Ala Pro
565 570 575

Glu Met Glu Arg Pro Pro Ala Pro Glu Ser Val Gly Thr Glu Glu Met
580 585 590

Pro Glu Asp Gly Glu Pro Asp Ala Ala Glu Leu Arg Arg Arg Arg Leu
595 600 605

Gln Lys Leu Glu Ser Pro Val Ala His
610 615

<210> 3
<211> 23
<212> DNA
<213> Homo sapiens

<400> 3
aatgtctgca tcatctgccg aga 23

<210> 4
<211> 23
<212> DNA
<213> Homo sapiens

<400> 4
aagctgtgac agatgccatc atg 23

<210> 5
<211> 23
<212> DNA
<213> Homo sapiens

<400> 5
aaagctgtga cagatccat cat 23

<210> 6
<211> 23
<212> DNA
<213> Homo sapiens

<400> 6
aagaaagctg tgacagatgc cat 23

<210> 7
<211> 23
<212> DNA
<213> Homo sapiens

<400> 7
aaggttctgc tgtacatggc ctt 23

<210> 8
<211> 23
<212> DNA
<213> Homo sapiens

<400> 8
aacaaggctg tgtacatgct cta

23

<210> 9
<211> 23
<212> DNA
<213> Homo sapiens

<400> 9
aaatgtttcc actggctggc tga

23

<210> 10
<211> 23
<212> DNA
<213> Homo sapiens

<400> 10
aagggtgttct ttgggcaact gag